Resource Summary Report

Generated by Kravitz on Sep 17, 2026

LDAK

RRID:SCR_015504
Type: Tool

Proper Citation

LDAK (RRID:SCR_015504)

Resource Information

URL: http://ldak.org/

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Description: Software that analyzes and estimates heritability. LDAK adjusts for linkage disequilibrium (LD) by calculating SNP weightings which downweight the contribution of SNPs in highly tagged regions.

Resource Type: data analysis software, data processing software, software application, software resource

Defining Citation: PMID:28530675

Keywords: linkage disequilibrium, ld, snp, snp weight, heritability

Availability: Free, Available for download

Resource Name: LDAK

Resource ID: SCR_015504

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260912T195827+0000

Ratings and Alerts

No rating or validation information has been found for LDAK.

No alerts have been found for LDAK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 124 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Wang P, et al. (2026) Heritability of Alzheimer's disease-related plasma biomarkers in the Amish population. Alzheimer's & dementia (Amsterdam, Netherlands), 18(2), e70388.

Chen X, et al. (2026) Comprehensive benchmarking single and multi ancestry polygenic score methods with the PGS-hub platform. Nature communications, 17(1).

Ueda H, et al. (2026) Elucidating genetic backgrounds of myasthenia gravis in Japanese by genome-wide association studies and multi-omics analyses of thymoma. Nature communications, 17(1).

Jade E, et al. (2026) An Increase in Male Recombination Rate With Age in Dairy Cattle Is Heritable and Polygenic. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 143(1), 35.

Mutz J, et al. (2026) Metabolomic ageing (MileAge) in mid-life predicts incident vascular, unspecified and all-cause dementia. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(5), e71280.

Berrandou TE, et al. (2026) Multi-trait and Gene-Based Analyses Identify Genetic Variants Associated with Spontaneous Coronary Artery Dissection. medRxiv : the preprint server for health sciences.

Lai D, et al. (2026) Genome-wide meta-analyses of cross substance use disorders in diverse populations. Molecular psychiatry, 31(3), 1619.

Wainschtein P, et al. (2026) Estimation and mapping of the missing heritability of human phenotypes. Nature, 649(8099), 1219.

Pan X, et al. (2026) Multi-Tissue Genetic Regulation of RNA Editing in Pigs. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e18238.

Yu J, et al. (2025) Identification of new candidate genes affecting drip loss in pigs based on genomics and transcriptomics data. Journal of animal science, 103.

Tabrizi F, et al. (2025) Heritability and polygenic load for comorbid anxiety and depression. Translational psychiatry, 15(1), 98.

Gautason E, et al. (2025) Haplotypes affecting stillbirth and fertility in Icelandic Dairy Cattle. Journal of applied genetics, 66(4), 1053.

Tiozon RN, et al. (2025) Lipidomics-based association study reveals genomic signatures of anti-cancer qualities of pigmented rice sprouts. Frontiers in plant science, 16, 1533442.

Hatzikotoulas K, et al. (2025) Translational genomics of osteoarthritis in 1,962,069 individuals. Nature, 641(8065), 1217.

Zhou J, et al. (2025) Integrated genome-wide association studies, meta-analysis, and Bayesian fine mapping reveal novel quantitative trait loci's and functional candidate genes for vulva traits in large white pigs. Journal of animal science, 103.

Toikumo S, et al. (2025) The cell-type-specific genetic architecture of chronic pain in brain and dorsal root ganglia. The Journal of clinical investigation, 135(24).

Rahimikollu J, et al. (2025) Multi-modal integration of protein interactomes with genomic and molecular data discovers distinct RA endotypes. medRxiv : the preprint server for health sciences.

Bracher-Smith M, et al. (2025) Machine learning in Alzheimer's disease genetics. Nature communications, 16(1), 6726.

Yang L, et al. (2025) Genetic association studies using disease liabilities from deep neural networks. American journal of human genetics, 112(3), 675.

Hayat M, et al. (2025) Genome-wide association study identifies common variants associated with breast cancer in South African Black women. Nature communications, 16(1), 3542.